

SEQUENCE LISTING

(1) GENERAL INFORMATION:

5 (i) APPLICANTS: Mark L. Gonzalgo and Peter A. Jones

(ii) TITLE OF INVENTION: A CANCER DIAGNOSTIC METHOD BASED UPON  
DNA METHYLATION DIFFERENCES

10 (iii) NUMBER OF SEQUENCES: 17

(iv) CORRESPONDENCE ADDRESS:

- (A) ADDRESSEE: DAVIS WRIGHT TREMAINE
- (B) STREET: 2600 Century Square, 1501 Fourth Avenue
- (C) CITY: Seattle
- (D) STATE: Washington
- (E) COUNTRY: U.S.A.
- (F) ZIP: 98101

20 (v) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: PC compatible
- (C) OPERATING SYSTEM: Windows95
- (D) SOFTWARE: Word

25 (vi) CURRENT APPLICATION DATA:

- (A) APPLICATION NUMBER: to be assigned
- (B) FILING DATE:
- (C) CLASSIFICATION:

30 (viii) ATTORNEY/AGENT INFORMATION:

- (A) NAME: Oster, Jeffrey B.
- (B) REGISTRATION NUMBER: 32,585
- (C) REFERENCE/DOCKET NUMBER: 47675-2

35 (ix) TELECOMMUNICATION INFORMATION:

- (A) TELEPHONE: 206 628 7711
- (B) TELEFAX: 206 628 7699

40 (2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 530
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: GaL1

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

1 CCCGCGACCT AAGCCAGCGA CTTACCACGT TAGTCAGCTA AGAAGTGGCA 50

51 GAGCTGGGAT TCGAACCTAT AAAGAACTCT GAAGCCTGGG TATTTTACA 100  
101 TGACACTTTA CATAATGCGC CACGGGGTAG TC GGAGGGGG AGGTCCATCT 150  
151 CCCTTCCCT TGCTGTCCAT CTCCACAGAA AAGAAGCAAG TGGAGGACAG 200  
201 GAGCCAGAAA GTCATCTGGC CGCGGATCAT TCCGGAGTGA CCCCCGCCGC 250  
5 251 CACCACTCGC ATAGTCCGCT TATGGCGGG A GGGCACCTCA GAGATTCTCA 300  
301 CAGGGCTGT GCGGCCAGAA CCAGAAGTGC AAAGCACCGT TAGCGACTCT 350  
351 ATCGCCCCCT GCCGCCTGTG GCGCCCAGTC CGAAGCTGCT GTTTTCAGGA 400  
401 GGGCTAGTGG GCTAAGAAAA GAGCTCACCG ACTGACTGCC CAACAGCTGT 450  
451 TGCGAGCCAG TGCTAGGCTG CAGACAGCCT TGCCAAATGT GGTGACATAA 500  
10 501 GCGGGAGGGG GGAACATTAA GAGAGCCCTA 530

(2) INFORMATION FOR SEQ ID NO:2:

15 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 308  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: unknown

20 (ii) MOLECULE TYPE: GaL2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

25 1 CTAGGGTAGG CTGGTCTGTG CTGGATACGC GTGTTCTTCT GCGGAGTTAA 50  
51 AGGGTCGGGG ACGGGGGTTG TGGACTTACC AGAGCAATTG CAGCCGGTGG 100  
101 GCGTTTGACA GCCACTTAAG GAGGTAGGGA AAGCGAGCTT CACCGGGCGG 150  
151 GCTACGATGA GTAGCATGAC GGGCAGCAGC AGCAGCAGCC AGCAAAAGCC 200  
201 TAGCAAAGTG TCCAGCTGCT GCACTGCCGC GGGGACTCCC ACATCACCAT 250  
251 GACTAGTTGT GCAACTCTGC AGCAGAAACG GCTTCCGAGG AACACAGGAT 300  
301 CGCGGGGG 308

(2) INFORMATION FOR SEQ ID NO:3:

35 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 177  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
40 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: GaL4

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

45 1 GCTTCCTTTT TCTCGGCTTT CCTCACTATC CTCTCCCTGT TCGAGAGTAT 50  
51 CTCCACCAGC ACCGAGCCTC ACACGGGCTG TGCCTCCATC TTTGGAATGC 100  
101 CTACCCCTCT TTCTTGCAGA GCCCCCTCCC GGGCCAGCCC TTGTGCACCG 150  
50 151 GCTCAAGGGG ACTGCTCTCC TGCCTCG 177

(2) INFORMATION FOR SEQ ID NO:4:

5 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 148
- (B) TYPE: oligonucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

10 (ii) MOLECULE TYPE: HuN1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

1 TTGCGCCGAT CGTCAAGAAC CTCTCATCCC TGGCAGCAGC AAAGCCAATA 50  
51 TATTTCATT TCTTATTTCAGTTGCCACC AAAACAAAGC TGCGCGCGGC 100  
101 TGAGGGCAGG AAGGCCTGA GACCGACCGA GAAGAAGGGGA CGTCCCCGG 148

15 (2) INFORMATION FOR SEQ ID NO:5:

20 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 384
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

25 (ii) MOLECULE TYPE: HuN2 primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

1 CAGGCCCGCC GAGACTCCAC TCCAATCACC AGGAAATTTC CCGTGGAGCT 50  
51 TCAATTCCCTG GGACCCTCCT ACTGCGGGGA GAGTGGTTTC CCTGCCAAC 100  
101 ACCATGCCCT AGGCCCGAGT CTGCGGCTCT TGGGGGATCT CTCCGAGCTC 150  
151 CGACACCGTG TTCGGACCGG GTGCGCCCTG CCGCTGGGC TCAAGCCTGC 200  
201 AGGCGTGAGA ACCGGGGGAC TCTCTATGGC ACCAAGAGCT TCACCGTGAG 250  
251 CGTAGGCAGA AGCTTCGCTT TGATCCTAGG GCTTACAAAG TCCTCCTTG 300  
301 GCTGCCCATG ATGGTAAAAG GGCAGTTGCT CACAAAGCGC GAGTGTGTGT 350  
351 GCCAGACAGT GTAAATGAGT GTTGGGACCG GCGT 384

35 (2) INFORMATION FOR SEQ ID NO:6:

40 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 178
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

45 (ii) MOLECULE TYPE: HuN3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

1 GGGTCCGTTG GTGAATGCAT GAGCAGGGTG TGAGGCCAG GGGGTTACAC 50  
51 TTCTCACGGG TTAAAACCCA GACAACCTCA CGAGGGAACC ACGTGCCATT 100  
50 101 TTAACAGCGT ACGGTCGGGA TCGTGGGACG TCATTAACG GAGTGGTTG 150  
151 AGTATGTGAC TCTGTCACCC ATTTTCTG

45 (2) INFORMATION FOR SEQ ID NO:7:

5 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 359
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

10 (ii) MOLECULE TYPE: HuN4 primer

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

20 1 CCCCGCGGGG CAGAATCCAA GTGAGTCAGA CACATTGCTC CCTCCCTGCT 50  
51 GCTGCCAGTC CATCTCTTG CCAACAAACC TGCTTAAAAT GCAAAGCTG 100  
101 GTCCAAAGTT TCAGGAAAAC AACTTCCGCC AGAGGGCACG TAGAGGGCAC 150  
151 AGATGCTATA GATGCTTCTC TGACAAACAC TCCTGACCCC CTTGACAGAT 200  
201 TGGAAAATAC ATGGTTCAGA AAGGGTGAGA GATTTCAACT TGAGAAGTGA 250  
251 AACTAGGAAA AGATGGAAGG TGTCCGGATT TCTAGCTCAA GTCCACACAC 300  
301 TGCTTCTGCT GCGGTGACTA AATCGTGGCT GTGTTCTCAT CACCTGCCTC 350  
351 GCGGCGCGC 359

25 (2) INFORMATION FOR SEQ ID NO:8:

30 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 251
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

35 (ii) MOLECULE TYPE: HuN5 primer

40 1 GGCGGGCCTG GGCACCGCGG AGGGGGGGCT TTTCTGCGCC CGCGAAGCG 50  
51 TGGAACTTGC GCCCTGAGGC AGCGCGCGA GACCAGTCCA GAGACCGGGG 100  
101 CGAGCCTCCT CAGGATTCCCT CGCCCCAGTG CAGATGCTGT GAGCTTAGAC 150  
151 GAGGACAGGG CATGGCACTC GGCTTGGCCC GTAGTGGACG GTGTTTTGC 200  
201 AGTCATGAAC CAAACCGCCG CAAACCTTGA CCGTTCCCC ACCCGTGTG T 251

45 (2) INFORMATION FOR SEQ ID NO:9:

50 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 145
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

55 (ii) MOLECULE TYPE: HuN6 primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

60 1 TGAGAGCAGC ATCCTCCCT GCGTGTGGTT CTCTAACTTA CCTCCTGTAT 50  
51 GGGGTCTGCG GACCCAGCAC ACCTCCGGG CCCCCAAAAA ATTCCAGCTC 100  
101 AAGAGCCCTA AAAATCCTTA CCCTGNNAAA GTTTGAGCTT CTCCC 145

65 (2) INFORMATION FOR SEQ ID NO:10:

5 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 215
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

10 (ii) MOLECULE TYPE: CaS1 primer

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

1 ACGCCGGCCA CAGTTCTTCA GTGAAACGCT TCACTCTCTG GTCATAGAGG 50  
51 TAGGAAACTA TAGCTGTCCC AACTAAATGT CAGGACGAAT TAGCCCAGCT 100  
101 GGTACCGCTC ACAGTCACCG CCTCCACCAG ACTGAGCGAC CCTCCCAACG 150  
151 GGGTTTGCCG TGTGGGAGG ACAGCGGAGT TTCGTTGCTG TGTCAATTG 200  
201 TGTAGACGCG GCTGC 215

20 (2) INFORMATION FOR SEQ ID NO:11:

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 220 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

30 (ii) MOLECULE TYPE: CaS2 primer

35 1 CTGCTCTCTT CTCTTCTTTT CCCCTTCCT CTCCTCTCCC TTTCCTCAGG 50  
51 TCACAGCGGA GTGAATCAGC TCGGTGGTGT CTTTGTCAAC GGGCGGCCAC 100  
101 TGCGGGACTC CACCCGGCAG AAGATTGTAG AGCTAGCTCA CAGCGGGGCC 150  
151 CGGCCGTGCG ACATTCTCCCG AATTCTGCAG GTGATCCTCC CGCGGCCGCC 200  
201 CCACTCGCCG CCCCCGGCGC 220

40 (2) INFORMATION FOR SEQ ID NO:12:

45 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 196
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

50 (ii) MOLECULE TYPE: CaS4 primer

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

60 1 GGGCGGCACG GAGGGAGTCA GGAGTGAGCC CGAAGATGGA GAGAAGTCGA 50  
51 TTTCGCCAGA GAACGCAAGA CGGTGGATCA GAGATGAGTC CCAGGAACCT 100  
101 CAGAGAGCGA GGCTGACAGG CCCGGGGAGA GGACCGGGCA GGGACAAACC 150  
151 AGCGGACAGA GCAGAGCGCG AAATGGTTGA GACCAGGAAG CGACCT 196

65 (2) INFORMATION FOR SEQ ID NO:13:

70 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

5 (ii) MOLECULE TYPE: Ms-SNuPE primer from *p16* promoter region

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

1 5'-GTA GGT GGG GAG GAG TTT AGT T-3' 22

10

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 23
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: unknown

20 (ii) MOLECULE TYPE: Ms-SNuPE primer from *p16* promoter region

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

25 1 5'-TCT AAT AAC CAA CCA ACC CCT CC-3

30 (2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 21
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: unknown

35 (ii) MOLECULE TYPE: Ms-SNuPE primer from *p16* promoter region

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

40 1 5'-TTT TTT TGT TTG GAA AGA TAT-3' 21

45

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 18
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: unknown

50 (ii) MOLECULE TYPE: Ms-SNuPE primer from *p16* promoter region

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

1 5'-TTT TAG GGG TGT TAT ATT-3' 18

(2) INFORMATION FOR SEQ ID NO:17:

5 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

10 (ii) MOLECULE TYPE: Ms-SNuPE primer from *p16* promoter region

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

15 1 5'-TTT GAG GGA TAG GGT-3' 15